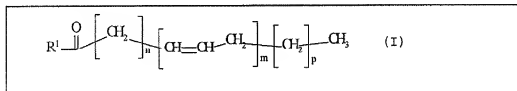


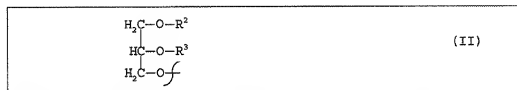
# AMENDMENTS TO THE CLAIMS

## Listing of Claims:

1. (Currently amended) A process for the production of compounds in transgenic plant cells, plants or parts thereof, wherein said compounds are comprised of general Formula I:



wherein  $R^1 = -OH$ , coenzyme A (thioester), phosphatidylcholine, phosphatidylethanolamine, phosphatidylglycerol, diphosphatidylglycerol, phosphatidylserine, phosphatidylinositol, sphingolipid, glycosphingolipid or a radical of general Formula II:



wherein  $R^2 =$  saturated or unsaturated  $C_{20}$ -alkylcarbonyl-; and  $R^3 =$  saturated or unsaturated  $C_{20}$ -alkylcarbonyl-;

wherein  $n = 3, 4$  or  $6$ ,  $m = 3, 4$  or  $5$ ; and  $p = 0$  or  $3$ , and said compounds comprise at least 1% by weight of the total fatty acid content of said transgenic plants, which process comprises the following steps:

introducing, into a plant cell, plant or part thereof:

at least one first nucleic acid sequence which encodes a polypeptide with an  $\Delta 6$ -desaturase activity;

at least one second nucleic acid sequence which encodes a polypeptide with a  $\Delta 6$ -elongase activity; and,

a third nucleic acid sequence which encodes a polypeptide with a  $\Delta 5$ -desaturase activity; and

growing and harvesting the transgenic plant cell, plant or part thereof.

wherein said nucleic acid sequences are obtained from *Phaeodactylum tricornutum* or *Physcomitrella patens*.

2-3. (Canceled).

4. (Previously presented) The process of claim 1, wherein  $R^2$  and  $R^3$  independently of one another are unsaturated  $C_{20}$ -alkylcarbonyl- with one, two, three, four or five double bonds.

5. (Previously presented) The process of claim 1, wherein the plant is an oil crop.

6. (Previously presented) The process of claim 1, wherein the plant is selected from the group consisting of soya, peanut, oilseed rape, canola, linseed, evening primrose, verbascum, thistle, hazelnut, almond, macadamia, avocado, bay, wild roses, pumpkin/squash, pistachios, sesame, sunflower, safflower, borage, maize, poppy, mustard, hemp, castor-oil plant, olive, Calendula, Punica, oil palm, walnut and coconut.

7. (Previously presented) The process of claim 1, wherein the compounds of general Formula I are obtained from the transgenic plants by pressing or extraction, and said compounds are in the form of oils, fats, lipids or free fatty acids.

8. (Previously presented) The process of claim 7, wherein the oils, fats, lipids or free fatty acids are refined.

9. (Previously presented) The process of claim 1, wherein saturated or unsaturated fatty acids present in the compounds are liberated.

10. (Previously presented) The process of claim 9, wherein the saturated or unsaturated fatty acids are liberated by alkaline hydrolysis or enzymatic cleavage.

11. (Previously presented) The process of claim 1, wherein the compounds comprise at least 5% by weight, of the total fatty acid content of the transgenic plants.

12. (Currently amended) The process of claim 1, wherein the nucleic acid sequence that encodes the polypeptide with  $\Delta 6$ -desaturase activity,  $\Delta 6$ -elongase activity or  $\Delta 5$ -desaturase activity comprises a nucleic acid sequence selected from the group consisting of:

- a) a nucleic acid sequence ~~that contains~~ comprising the sequence of SEQ ID NO: 1, SEQ ID NO: 3, ~~SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11,~~

SEQ ID NO: 13, ~~SEQ ID NO: 15~~, SEQ ID NO: 17, or ~~SEQ ID NO: 19~~, SEQ ID NO: 21, ~~SEQ ID NO: 23~~, ~~SEQ ID NO: 25~~, ~~SEQ ID NO: 27~~, ~~SEQ ID NO: 29~~ or SEQ ID NO: 31,

- b) a nucleic acid sequence encoding a polypeptide comprising the amino acid sequence of ~~SEQ ID NO: 2~~, SEQ ID NO: 4, ~~SEQ ID NO: 6~~, ~~SEQ ID NO: 8~~, ~~SEQ ID NO: 10~~, ~~SEQ ID NO: 12~~, SEQ ID NO: 14, ~~SEQ ID NO: 16~~, SEQ ID NO: 18, or ~~SEQ ID NO: 20~~, SEQ ID NO: 22, ~~SEQ ID NO: 24~~, ~~SEQ ID NO: 26~~, ~~SEQ ID NO: 28~~, ~~SEQ ID NO: 30~~ or ~~SEQ ID NO: 32~~, and
- c) a nucleic acid sequence encoding a polypeptide having at least 90% homology with the amino acid sequence of ~~SEQ ID NO: 2~~, SEQ ID NO: 4, ~~SEQ ID NO: 6~~, ~~SEQ ID NO: 8~~, ~~SEQ ID NO: 10~~, ~~SEQ ID NO: 12~~, SEQ ID NO: 14, ~~SEQ ID NO: 16~~, SEQ ID NO: 18, or ~~SEQ ID NO: 20~~, SEQ ID NO: 22, ~~SEQ ID NO: 24~~, ~~SEQ ID NO: 26~~, ~~SEQ ID NO: 28~~, ~~SEQ ID NO: 30~~ or ~~SEQ ID NO: 32~~; wherein the polypeptide has essentially the same enzymatic activity.

13. (Currently amended) The process of claim 1, wherein one or more of the first, second, and ~~optionally~~ third nucleic acid sequences are linked with one or more regulatory signals in a nucleic acid construct.

14. (Previously presented) The process of claim 13, wherein the nucleic acid construct comprises additional biosynthetic genes of fatty acid or lipid metabolism selected from the group consisting of acyl-CoA dehydrogenase(s), acyl-ACP [= acyl carrier protein] desaturase(s), acyl-ACP thioesterase(s), fatty acid acyl transferase(s), fatty acid synthase(s), fatty acid hydroxylase(s), acetyl-coenzyme A carboxylase(s), acyl-coenzyme A oxidase(s), fatty acid desaturase(s), fatty acid acetylases, lipoxigenases, triacylglycerol lipases, allene oxide synthases, hydroperoxide lyases fatty acid elongase(s) and combinations thereof.

15. (Currently amended) The process of claim 1, wherein the first, second and ~~optionally~~ third nucleic acid sequences are stably integrated in the plant.

16. (Currently amended) The process of claim 1, wherein the plant or part thereof is selected from the group consisting of plant cells, comprises plant tissues, plant organs, plant leaves, plant

roots, plant stems, intact plants, plant ~~tubers~~ tubers, plant seeds, and or cellular parts of any of the preceding.

17. (Previously presented) The process of claim 7, wherein the pressing or the extraction is performed without supplying heat.

18. (Previously presented) The process of claim 12, wherein two or more of the first, second and third nucleic acid sequences are selected from the group of nucleic acid sequences as set forth in claim 12.

19. (Previously presented) The process of claim 12, wherein the first, second and third nucleic acid sequences are selected from the group of nucleic acid sequences as set forth in claim 12.

20. (Previously presented) The process of claim 13, wherein the first, second and third nucleic acid sequences are linked with one or more regulatory signals in said nucleic acid construct.

21. (Previously presented) The process of claim 1, wherein the plant is a dicot.

22. (Previously presented) The process of claim 1, wherein the plant is tobacco or linseed.